



OIPE

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/077,130

DATE: 03/04/2002

TIME: 14:49:08

Input Set : A:\Seq Listing.txt

Output Set: N:\CRF3\03042002\J077130.raw

4 <110> APPLICANT: Kapeller-Libermann, Rosana
 5 Acton, Susan L.
 7 <120> TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
 8 Members and Uses Therefor
 11 <130> FILE REFERENCE: MPI2001-047P1RCP1(M)
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/077,130
 C--> 13 <141> CURRENT FILING DATE: 2002-02-15
 13 <150> PRIOR APPLICATION NUMBER: 60/269201
 14 <151> PRIOR FILING DATE: 2001-02-15
 16 <160> NUMBER OF SEQ ID NOS: 9
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 8106
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: 5'UTR
 27 <222> LOCATION: (1)...(71)
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (72)...(7964)
 32 <221> NAME/KEY: 3'UTR
 33 <222> LOCATION: (7965)...(8106)
 35 <400> SEQUENCE: 1
 36 tgcacaccct ggagatcatc tccgtcacc cggaggactc tggccagtat gcagcctata 60
 37 tcagcaatgc c atg ggt gct gcc tac tgc tct gcc cgg ctg ctg gtt cga 110
 38 Met Gly Ala Ala Tyr Ser Ser Ala Arg Leu Leu Val Arg
 39 1 5 10
 41 ggc cct gat gag cca gaa gag aag cct gca tca gat gtg cat gag cag 158
 42 Gly Pro Asp Glu Pro Glu Glu Lys Pro Ala Ser Asp Val His Glu Gln
 43 15 20 25
 45 ctg gtg ccg ccc cga atg ctg gag agg ttc acc ccc aag aaa gtg aag 206
 46 Leu Val Pro Pro Arg Met Leu Glu Arg Phe Thr Pro Lys Lys Val Lys
 47 30 35 40 45
 49 aaa ggc tcc agc atc acc ttc tct gtg aag gta gaa gga cgc ccg gtg 254
 50 Lys Gly Ser Ser Ile Thr Phe Ser Val Lys Val Glu Gly Arg Pro Val
 51 50 55 60
 53 ccc acc gtg cac tgg ctg agg gag gag gct gag aga ggc gtg ctg tgg 302
 54 Pro Thr Val His Trp Leu Arg Glu Glu Ala Glu Arg Gly Val Leu Trp
 55 65 70 75
 57 att ggc cct gac aca ccg ggc tac acc gtg gcc agc tct gcg cag cag 350
 58 Ile Gly Pro Asp Thr Pro Gly Tyr Thr Val Ala Ser Ser Ala Gln Gln
 59 80 85 90
 61 cac agc ctg gtc ctg ctg gac gtg ggc cgg cag cac cag ggc acc tac 398

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62 His Ser Leu Val Leu Leu Asp Val Gly Arg Gln His Gln Gly Thr Tyr
63      95      100      105
65 aca tgc att gcc agc aac gct gcc ggc cag gcc ctc tgc tcc gcc agc 446
66 Thr Cys Ile Ala Ser Asn Ala Ala Gly Gln Ala Leu Cys Ser Ala Ser
67 110      115      120      125
69 ctg cac gtc tcg ggc ctg cct aag gtg gag gag cag gag aaa gtg aag 494
70 Leu His Val Ser Gly Leu Pro Lys Val Glu Glu Gln Glu Lys Val Lys
71      130      135      140
73 gaa gcg ctg att tcc act ttc ctg cag ggg acc aca caa gcc atc tca 542
74 Glu Ala Leu Ile Ser Thr Phe Leu Gln Gly Thr Thr Gln Ala Ile Ser
75      145      150      155
77 gca cag ggg ttg gaa act gcg agt ttt gct gac ctt ggt ggg cag agg 590
78 Ala Gln Gly Leu Glu Thr Ala Ser Phe Ala Asp Leu Gly Gly Gln Arg
79      160      165      170
81 aaa gaa gag cct ctg gct gcc aag gag gcc ctc ggc cac ctg tcc ctc 638
82 Lys Glu Glu Pro Leu Ala Ala Lys Glu Ala Leu Gly His Leu Ser Leu
83      175      180      185
85 gct gag gtg ggc aca gag gag ttc ctg cag aaa ctg acc tcc cag atc 686
86 Ala Glu Val Gly Thr Glu Glu Phe Leu Gln Lys Leu Thr Ser Gln Ile
87 190      195      200      205
89 act gag atg gta tcg gcc aag atc acg cag gcc aag ctg cag gtg ccc 734
90 Thr Glu Met Val Ser Ala Lys Ile Thr Gln Ala Lys Leu Gln Val Pro
91      210      215      220
93 gga ggt gac agt gat gag gac tcc aag aca cca tct gca tcc ccc cgc 782
94 Gly Gly Asp Ser Asp Glu Asp Ser Lys Thr Pro Ser Ala Ser Pro Arg
95      225      230      235
97 cat ggc cga tca cgg cca tcc tcc agc atc cag gag tct tcc tca gag 830
98 His Gly Arg Ser Arg Pro Ser Ser Ser Ile Gln Glu Ser Ser Ser Glu
99      240      245      250
101 tca gag gac ggc gat gcc cga ggc gag atc ttt gac atc tac gtg gtc 878
102 Ser Glu Asp Gly Asp Ala Arg Gly Glu Ile Phe Asp Ile Tyr Val Val
103      255      260      265
105 acc gct gac tac ctg ccc cta ggg gct gag cag gat gcc atc acg ctg 926
106 Thr Ala Asp Tyr Leu Pro Leu Gly Ala Glu Gln Asp Ala Ile Thr Leu
107 270      275      280      285
109 cgg gaa ggc cag tat gtg gag gtc ctg gat gca gcc cac cca ctg cgc 974
110 Arg Glu Gly Gln Tyr Val Glu Val Leu Asp Ala Ala His Pro Leu Arg
111      290      295      300
113 tgg ctt gtc cgc acc aag ccc acc aag tcc agc ccc tca cgg cag gcc 1022
114 Trp Leu Val Arg Thr Lys Pro Thr Lys Ser Ser Pro Ser Arg Gln Gly
115      305      310      315
117 tgg gtg tca cca gcc tac ctg gac agg agg ctc aag ctg tca cct gag 1070
118 Trp Val Ser Pro Ala Tyr Leu Asp Arg Arg Leu Lys Leu Ser Pro Glu
119      320      325      330
121 tgg ggg gcc gct gag gcc cct gag ttc cct ggg gag gct gtg tct gaa 1118
122 Trp Gly Ala Ala Glu Ala Pro Glu Phe Pro Gly Glu Ala Val Ser Glu
123      335      340      345
125 gac gaa tac aag gca agg ctg agc tct gtg atc cag gag ctg ctg agt 1166
126 Asp Glu Tyr Lys Ala Arg Leu Ser Ser Val Ile Gln Glu Leu Leu Ser

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127	350				355				360				365				
129	tct	gag	cag	gcc	ttc	gtg	gag	gag	ctg	cag	ttc	ctg	cag	agc	cac	cac	1214
130	Ser	Glu	Gln	Ala	Phe	Val	Glu	Glu	Leu	Gln	Phe	Leu	Gln	Ser	His	His	
131					370				375				380				
133	ctg	cag	cac	ctg	gag	cgc	tgc	ccc	cac	gtg	ccc	ata	gcc	gtg	gcc	ggc	1262
134	Leu	Gln	His	Leu	Glu	Arg	Cys	Pro	His	Val	Pro	Ile	Ala	Val	Ala	Gly	
135				385					390				395				
137	cag	aag	gca	gtc	atc	ttc	cgc	aat	gtg	cgg	gac	atc	ggc	cgc	ttc	cac	1310
138	Gln	Lys	Ala	Val	Ile	Phe	Arg	Asn	Val	Arg	Asp	Ile	Gly	Arg	Phe	His	
139			400					405					410				
141	agc	agc	ttc	ctg	cag	gag	ttg	cag	cag	tgc	gac	acg	gac	gac	gac	gtg	1358
142	Ser	Ser	Phe	Leu	Gln	Glu	Leu	Gln	Gln	Cys	Asp	Thr	Asp	Asp	Asp	Val	
143			415				420						425				
145	gcc	atg	tgc	ttc	atc	aag	aac	cag	gcg	gcc	ttt	gag	cag	tac	ctg	gag	1406
146	Ala	Met	Cys	Phe	Ile	Lys	Asn	Gln	Ala	Ala	Phe	Glu	Gln	Tyr	Leu	Glu	
147	430					435					440					445	
149	ttc	ctg	gtg	ggg	cgt	gtg	cag	gct	gag	tcg	gtg	gtc	gtc	agc	acg	gcc	1454
150	Phe	Leu	Val	Gly	Arg	Val	Gln	Ala	Glu	Ser	Val	Val	Val	Ser	Thr	Ala	
151				450					455					460			
153	atc	cag	gag	ttc	tac	aag	aaa	tac	gcg	gag	gag	gcc	ctg	ttg	gca	ggg	1502
154	Ile	Gln	Glu	Phe	Tyr	Lys	Lys	Tyr	Ala	Glu	Glu	Ala	Leu	Leu	Ala	Gly	
155			465					470					475				
157	gac	ccc	tct	cag	ccc	ccg	cca	cca	cct	ctg	cag	cac	tac	ctg	gag	cag	1550
158	Asp	Pro	Ser	Gln	Pro	Pro	Pro	Pro	Pro	Leu	Gln	His	Tyr	Leu	Glu	Gln	
159			480					485					490				
161	cca	gtg	gag	cgg	gtg	cag	cgc	tac	cag	gcc	ttg	ctg	aag	gag	ttg	atc	1598
162	Pro	Val	Glu	Arg	Val	Gln	Arg	Tyr	Gln	Ala	Leu	Leu	Lys	Glu	Leu	Ile	
163		495					500						505				
165	cgc	aac	aag	gcg	cgg	aac	aga	cag	aac	tgc	gcg	ctg	ctg	gag	cag	gcc	1646
166	Arg	Asn	Lys	Ala	Arg	Asn	Arg	Gln	Asn	Cys	Ala	Leu	Leu	Glu	Gln	Ala	
167	510					515					520					525	
169	tat	gcc	gtg	gtg	tct	gcc	ctg	cca	cag	cgc	gct	gag	aac	aag	ctg	cac	1694
170	Tyr	Ala	Val	Val	Ser	Ala	Leu	Pro	Gln	Arg	Ala	Glu	Asn	Lys	Leu	His	
171					530					535					540		
173	gtg	tcc	ctc	atg	gag	aac	tac	cca	ggc	acc	ctg	gag	gcc	ctg	ggc	gag	1742
174	Val	Ser	Leu	Met	Glu	Asn	Tyr	Pro	Gly	Thr	Leu	Glu	Ala	Leu	Gly	Glu	
175				545					550					555			
177	ccc	atc	cgc	cag	ggc	cac	ttc	atc	gtg	tgg	gag	ggt	gca	ccg	ggg	gcc	1790
178	Pro	Ile	Arg	Gln	Gly	His	Phe	Ile	Val	Trp	Glu	Gly	Ala	Pro	Gly	Ala	
179			560					565					570				
181	cgc	atg	ccc	tgg	aag	ggc	cac	aac	cgt	cac	gtg	ttc	ctc	ttc	cgc	aac	1838
182	Arg	Met	Pro	Trp	Lys	Gly	His	Asn	Arg	His	Val	Phe	Leu	Phe	Arg	Asn	
183		575				580						585					
185	cac	ctg	gta	atc	tgc	aag	ccc	cgg	cga	gac	tcc	cgc	acc	gat	acc	gtc	1886
186	His	Leu	Val	Ile	Cys	Lys	Pro	Arg	Arg	Asp	Ser	Arg	Thr	Asp	Thr	Val	
187	590					595					600					605	
189	agc	tac	gtg	ttc	cgg	aac	atg	atg	aag	ctg	agc	agc	atc	gac	ctg	aac	1934
190	Ser	Tyr	Val	Phe	Arg	Asn	Met	Met	Lys	Leu	Ser	Ser	Ile	Asp	Leu	Asn	
191					610					615						620	

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```

193 gac cag gtg gag ggg gat gac cgc gcc ttc gag gtg tgg cag gag cgg 1982
194 Asp Gln Val Glu Gly Asp Asp Arg Ala Phe Glu Val Trp Gln Glu Arg
195 625 630 635
197 gag gac tcg gtg cgc aag tac ctg ctg cag gca cgg aca gcc att atc 2030
198 Glu Asp Ser Val Arg Lys Tyr Leu Leu Gln Ala Arg Thr Ala Ile Ile
199 640 645 650
201 aag agc tcg tgg gtg aag gag atc tgt ggc atc cag cag cgt ctg gcc 2078
202 Lys Ser Ser Trp Val Lys Glu Ile Cys Gly Ile Gln Gln Arg Leu Ala
203 655 660 665
205 ctg cct gtg tgg cgg ccc ccg gac ttt gaa gag gag ctg gcc gac tgc 2126
206 Leu Pro Val Trp Arg Pro Pro Asp Phe Glu Glu Glu Leu Ala Asp Cys
207 670 675 680 685
209 aca gcc gag ctg ggt gag aca gtc aag ctg gcc tgc cgc gtg acg ggc 2174
210 Thr Ala Glu Leu Gly Glu Thr Val Lys Leu Ala Cys Arg Val Thr Gly
211 690 695 700
213 aca ccc aag cct gtc atc agc tgg tac aaa gat ggg aaa gca gtg cag 2222
214 Thr Pro Lys Pro Val Ile Ser Trp Tyr Lys Asp Gly Lys Ala Val Gln
215 705 710 715
217 gtg gac ccc cac cac atc ctc att gaa gac cct gat ggc tcg tgt gca 2270
218 Val Asp Pro His His Ile Leu Ile Glu Asp Pro Asp Gly Ser Cys Ala
219 720 725 730
221 ctc atc ctg gac agc ctg acc ggt gtg gac tct ggc cag tac atg tgc 2318
222 Leu Ile Leu Asp Ser Leu Thr Gly Val Asp Ser Gly Gln Tyr Met Cys
223 735 740 745
225 ttc gcg gcc agc gcc gct ggc aac tgc agt acc ctg ggc aag atc ctg 2366
226 Phe Ala Ala Ser Ala Ala Gly Asn Cys Ser Thr Leu Gly Lys Ile Leu
227 750 755 760 765
229 gtg caa gtc cca cca cgg ttc gtg aac aag gtc cgg gcc tca ccc ttt 2414
230 Val Gln Val Pro Pro Arg Phe Val Asn Lys Val Arg Ala Ser Pro Phe
231 770 775 780
233 gtg gag gga gag gac gcc cag ttc acc tgc acc atc gaa ggc gcc ccg 2462
234 Val Glu Gly Glu Asp Ala Gln Phe Thr Cys Thr Ile Glu Gly Ala Pro
235 785 790 795
237 tac ccg cag atc agg tgg tac aag gac ggg gcc ctg ctg acc act ggc 2510
238 Tyr Pro Gln Ile Arg Trp Tyr Lys Asp Gly Ala Leu Leu Thr Thr Gly
239 800 805 810
241 aac aag ttc cag aca ctg agt gag cct cgc agc ggc ctg cta gtg ctg 2558
242 Asn Lys Phe Gln Thr Leu Ser Glu Pro Arg Ser Gly Leu Leu Val Leu
243 815 820 825
245 gtg atc cgg gcg gcc agc aag gag gac ctg ggg ctc tac gag tgt gag 2606
246 Val Ile Arg Ala Ala Ser Lys Glu Asp Leu Gly Leu Tyr Glu Cys Glu
247 830 835 840 845
249 ctg gtg aac cgg ctg ggc tcc gcg cgg gct agt gcg gag ctg cgc att 2654
250 Leu Val Asn Arg Leu Gly Ser Ala Arg Ala Ser Ala Glu Leu Arg Ile
251 850 855 860
253 cag agc ccc atg ctg cag gcc cag gag cag tgt cac agg gag cag ctc 2702
254 Gln Ser Pro Met Leu Gln Ala Gln Glu Gln Cys His Arg Glu Gln Leu
255 865 870 875
257 gtg gct gca gtg gaa gac acc acc ctg gag cga gcg gac cag gag gtc 2750

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258 Val Ala Ala Val Glu Asp Thr Thr Leu Glu Arg Ala Asp Gln Glu Val
259      880      885      890
261 aca tct gtc ctg aag aga ctg ctg ggc ccc aag gcg cca ggc ccc tcc 2798
262 Thr Ser Val Leu Lys Arg Leu Leu Gly Pro Lys Ala Pro Gly Pro Ser
263      895      900      905
265 aca ggg gac ctc act ggc cct ggc ccc tgc ccc agg ggg gca ccc gca 2846
266 Thr Gly Asp Leu Thr Gly Pro Gly Pro Cys Pro Arg Gly Ala Pro Ala
267 910      915      920      925
269 ctc cag gaa acc ggc tcc cag ccc cca gtc acc gga act tcg gag gca 2894
270 Leu Gln Glu Thr Gly Ser Gln Pro Pro Val Thr Gly Thr Ser Glu Ala
271      930      935      940
273 cct gcc gtg ccc ccg agg gtg cca cag ccc ctc ctc cac gaa ggc cca 2942
274 Pro Ala Val Pro Pro Arg Val Pro Gln Pro Leu Leu His Glu Gly Pro
275      945      950      955
277 gag cag gag ccg gag gcc att gcc aga gcc cag gaa tgg act gtg ccc 2990
278 Glu Gln Glu Pro Glu Ala Ile Ala Arg Ala Gln Glu Trp Thr Val Pro
279      960      965      970
281 att cgg atg gag ggt gca gcc tgg ccc ggg gca ggc aca ggg gag ctg 3038
282 Ile Arg Met Glu Gly Ala Ala Trp Pro Gly Ala Gly Thr Gly Glu Leu
283      975      980      985
285 ctc tgg gac gtc cac agc cac gtg gtc aga gag acc aca cag agg acc 3086
286 Leu Trp Asp Val His Ser His Val Val Arg Glu Thr Thr Gln Arg Thr
287 990      995      1000      1005
289 tac aca tac cag gcc atc gac acg cac acc gca cgg ccc cca tcc atg 3134
290 Tyr Thr Tyr Gln Ala Ile Asp Thr His Thr Ala Arg Pro Pro Ser Met
291      1010      1015      1020
293 cag gta acc atc gag gat gtg cag gca cag aca ggc gga acg gcc caa 3182
294 Gln Val Thr Ile Glu Asp Val Gln Ala Gln Thr Gly Gly Thr Ala Gln
295      1025      1030      1035
297 ttc gag gct atc att gag ggc gac cca cag ccc tcg gtg acc tgg tac 3230
298 Phe Glu Ala Ile Ile Glu Gly Asp Pro Gln Pro Ser Val Thr Trp Tyr
299      1040      1045      1050
301 aag gac agc gtc cag ctg gtg gac agc acc cgg ctt agc cag cag caa 3278
302 Lys Asp Ser Val Gln Leu Val Asp Ser Thr Arg Leu Ser Gln Gln Gln
303      1055      1060      1065
305 gaa ggc acc aca tac tcc ctg gtg ctg agg cat gtg gcc tcg aag gat 3326
306 Glu Gly Thr Thr Tyr Ser Leu Val Leu Arg His Val Ala Ser Lys Asp
307 1070      1075      1080      1085
309 gcc ggc gtt tac acc tgc ctg gcc caa aac act ggt ggc cag gtg ctc 3374
310 Ala Gly Val Tyr Thr Cys Leu Ala Gln Asn Thr Gly Gly Gln Val Leu
311      1090      1095      1100
313 tgc aag gca gag ctg ctg gtg ctt ggg ggg gac aat gag ccg gac tca 3422
314 Cys Lys Ala Glu Leu Leu Val Leu Gly Gly Asp Asn Glu Pro Asp Ser
315      1105      1110      1115
317 gag aag caa agc cac cgg agg aag ctg cac tcc ttc tat gag gtc aag 3470
318 Glu Lys Gln Ser His Arg Arg Lys Leu His Ser Phe Tyr Glu Val Lys
319      1120      1125      1130
321 gag gag att gga agg ggc gtg ttt ggc ttc gta aaa aga gtg cag cac 3518
322 Glu Glu Ile Gly Arg Gly Val Phe Gly Phe Val Lys Arg Val Gln His

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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\Seq Listing.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:4686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:4735 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:4739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:4793 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:4797 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9